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RAW SEQUENCE LISTING

DATE: 04/16/2002

PATENT APPLICATION: US/09/308,830A

TIME: 11:31:36

Input Set : A:\600-346SeqLst.txt

Output Set: N:\CRF3\04162002\I308830A.raw

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3 <110> APPLICANT: Schlievert, Patrick M.
4   Roggiani, Manuela
5   Auge, Jennifer Stoehr
6   Ohlendorf, Douglas
8 <120> TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
10 <130> FILE REFERENCE: 600.346USWO
12 <140> CURRENT APPLICATION NUMBER: US 09/308,830A
13 <141> CURRENT FILING DATE: 1999-08-04
15 <150> PRIOR APPLICATION NUMBER: PCT/US97/22228
16 <151> PRIOR FILING DATE: 1997-12-05
18 <150> PRIOR APPLICATION NUMBER: US 60/032,930
19 <151> PRIOR FILING DATE: 1996-12-06
21 <160> NUMBER OF SEQ ID NOS: 13
23 <170> SOFTWARE: PatentIn version 3.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 29
27 <212> TYPE: DNA
28 <213> ORGANISM: Streptococcus sp.
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36 <212> TYPE: DNA
37 <213> ORGANISM: Streptococcus sp.
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45 <212> TYPE: DNA
46 <213> ORGANISM: Streptococcus sp.
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51 taaatatata aataaaataa ttacatatata aaaataatac ttaattataa aaacactata    120
53 atttccataa atattaataa ataattaaaa ataaaataat aaataattaa tc             172
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59 <213> ORGANISM: Streptococcus sp.
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69 <210> SEQ ID NO: 5

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77 taaatatata aataaaataa ttacatatta aaaataatac ttaattataa aaacactata      120
79 atttccataa atattaataa ataattaaaa ataaaataat aaataattaa tc              172
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83 <211> LENGTH: 172
84 <212> TYPE: DNA
85 <213> ORGANISM: Streptococcus sp.
87 <400> SEQUENCE: 6
88 ccatcaccat caccaagaag aaataattac atattaaata caatacatat gtaataataa      60
90 taaatatata aataaaataa ttacatatta aaaataatac ttaattataa aaacactata      120
92 atttccataa atattaataa ataattaaaa ataaaataat aaataattaa tc              172
95 <210> SEQ ID NO: 7
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97 <212> TYPE: DNA
98 <213> ORGANISM: Streptococcus sp.
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101 ccatcaccat caccaagaag aaataattac atattaaata caatacatat gtaataataa      60
103 taaatatata aataaaataa ttacatatta aaaataatac ttaattataa aaacactata      120
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108 <210> SEQ ID NO: 8
109 <211> LENGTH: 172
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111 <213> ORGANISM: Streptococcus sp.
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121 <210> SEQ ID NO: 9
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126 <400> SEQUENCE: 9
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147 <210> SEQ ID NO: 11
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159 <213> ORGANISM: Streptococcus sp.
161 <220> FEATURE:
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163 <222> LOCATION: (828)..(1580)
164 <223> OTHER INFORMATION:
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170 tctatccttg aaacaggtgc aacatagatt agggcatgga gatttaccag acaactatga 120
172 acgtatatac tcacatcacg caatcggaac ttgatgacat tggaaactaaa ttcaatcaat 180
174 ttgttactaa caagcaacta gattgacaac taattctcaa caaacgttaa tttacaaca 240
176 ttcaagtaac tcccaccagc tccatcaatg cttaccgtaa gtaatcataa cttactaaaa 300
178 ccttggttaca tcaagggtttt ttctttttgt cttgttcatg agttaccata actttctata 360
180 ttattgacaa ctaaattgac aactcttcaa ttatttttct gtctactcaa agttttcttc 420
182 atttgatata gtctaattcc accatcactt cttccactct ctctaccgtc acaacttcat 480
184 catctctcac tttttcgtgt ggtaacacat aatcaaatat ctttccggtt ttacgcacta 540
186 tcgtactgt gtcacctaaa atatacccct tatcaatcgc ttctttaaac tcatctatat 600
188 ataacatatt tcatcctcct acctatctat tcgtaaaaag ataaaaataa ctattgtttt 660
190 ttttggttatt ttataataaa attattaata taagttaatg ttttttaaaa atatacaatt 720
192 ttattctatt tatagttagc tattttttca ttgttagtaa tattggtgaa ttgtaataac 780
194 ctttttaaat ctagaggaga acccagatat aaaatggagg aatatta atg gaa aac 836
195 Met Glu Asn
196 1
198 aat aaa aaa gta ttg aag aaa atg gta ttt ttt gtt tta gtg aca ttt 884
199 Asn Lys Lys Val Leu Lys Lys Met Val Phe Phe Val Leu Val Thr Phe
200 5 10 15
202 ctt gga cta aca atc tcg caa gag gta ttt gct caa caa gac ccc gat 932
203 Leu Gly Leu Thr Ile Ser Gln Glu Val Phe Ala Gln Gln Asp Pro Asp
204 20 25 30 35
206 cca agc caa ctt cac aga tct agt tta gtt aaa aac ctt caa aat ata 980
207 Pro Ser Gln Leu His Arg Ser Ser Leu Val Lys Asn Leu Gln Asn Ile
208 40 45 50
210 tat ttt ctt tat gag ggt gac cct gtt act cac gag aat gtg aaa tct 1028
211 Tyr Phe Leu Tyr Glu Gly Asp Pro Val Thr His Glu Asn Val Lys Ser
212 55 60 65
214 gtt gat caa ctt tta tct cac cat tta ata tat aat gtt tca ggg cca 1076
215 Val Asp Gln Leu Leu Ser His His Leu Ile Tyr Asn Val Ser Gly Pro
216 70 75 80
218 aat tat gat aaa tta aaa act gaa ctt aag aac caa gag atg gca act 1124
219 Asn Tyr Asp Lys Leu Lys Thr Glu Leu Lys Asn Gln Glu Met Ala Thr
220 85 90 95
222 tta ttt aag gat aaa aac gtt gat att tat ggt gta gaa tat tac cat 1172
223 Leu Phe Lys Asp Lys Asn Val Asp Ile Tyr Gly Val Glu Tyr Tyr His

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224 100          105          110          115
226 ctc tgt tat tta tgt gaa aat gca gaa agg agt gca tgt atc tac gga      1220
227 Leu Cys Tyr Leu Cys Glu Asn Ala Glu Arg Ser Ala Cys Ile Tyr Gly
228          120          125          130
230 ggg gta aca aat cat gaa ggg aat cat tta gaa att cct aaa aag ata      1268
231 Gly Val Thr Asn His Glu Gly Asn His Leu Glu Ile Pro Lys Lys Ile
232          135          140          145
234 gtc gtt aaa gta tca atc gat ggt atc caa agc cta tca ttt gat att      1316
235 Val Val Lys Val Ser Ile Asp Gly Ile Gln Ser Leu Ser Phe Asp Ile
236          150          155          160
238 gaa aca aat aaa aaa atg gta act gct caa gaa tta gac tat aaa gtt      1364
239 Glu Thr Asn Lys Lys Met Val Thr Ala Gln Glu Leu Asp Tyr Lys Val
240          165          170          175
242 aga aaa tat ctt aca gat aat aag caa cta tat act aat gga cct tct      1412
243 Arg Lys Tyr Leu Thr Asp Asn Lys Gln Leu Tyr Thr Asn Gly Pro Ser
244 180          185          190          195
246 aaa tat gaa act gga tat ata aag ttc ata cct aag aat aaa gaa agt      1460
247 Lys Tyr Glu Thr Gly Tyr Ile Lys Phe Ile Pro Lys Asn Lys Glu Ser
248          200          205          210
250 ttt tgg ttt gat ttt ttc cct gaa cca gaa ttt act caa tct aaa tat      1508
251 Phe Trp Phe Asp Phe Phe Pro Glu Pro Glu Phe Thr Gln Ser Lys Tyr
252          215          220          225
254 ctt atg ata tat aaa gat aat gaa acg ctt gac tca aac aca agc caa      1556
255 Leu Met Ile Tyr Lys Asp Asn Glu Thr Leu Asp Ser Asn Thr Ser Gln
256          230          235          240
258 att gaa gtc tac cta aca acc aag taacttttttg ctttttgcaa ccttacctac      1610
259 Ile Glu Val Tyr Leu Thr Thr Lys
260          245          250
262 tgctggatttt agaaatttta ttgcaattct tttattaatg taaaaaacgc tcatttgatg      1670
264 agcgggttttg tcttatctaa aggagcttta cctcctaag ctgcaaaatt ttaaatgttg      1730
266 gatttttgta tttgtctatt gtatttgatg ggtaatccca tttttcgaca gacatcgtcg      1790
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275 <212> TYPE: PRT
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281 1          5          10          15
284 Val Thr Phe Leu Gly Leu Thr Ile Ser Gln Glu Val Phe Ala Gln Gln
285          20          25          30
288 Asp Pro Asp Pro Ser Gln Leu His Arg Ser Ser Leu Val Lys Asn Leu
289          35          40          45
292 Gln Asn Ile Tyr Phe Leu Tyr Glu Gly Asp Pro Val Thr His Glu Asn
293          50          55          60
296 Val Lys Ser Val Asp Gln Leu Leu Ser His His Leu Ile Tyr Asn Val
297 65          70          75          80
300 Ser Gly Pro Asn Tyr Asp Lys Leu Lys Thr Glu Leu Lys Asn Gln Glu

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305				100					105				110
308	Tyr	Tyr	His	Leu	Cys	Tyr	Leu	Cys	Glu	Asn	Ala	Glu	Arg
309			115						120				125
312	Ile	Tyr	Gly	Gly	Val	Thr	Asn	His	Glu	Gly	Asn	His	Leu
313		130							135				140
316	Lys	Lys	Ile	Val	Val	Lys	Val	Ser	Ile	Asp	Gly	Ile	Gln
317	145						150				155		160
320	Phe	Asp	Ile	Glu	Thr	Asn	Lys	Lys	Met	Val	Thr	Ala	Gln
321					165					170			175
324	Tyr	Lys	Val	Arg	Lys	Tyr	Leu	Thr	Asp	Asn	Lys	Gln	Leu
325			180						185				190
328	Gly	Pro	Ser	Lys	Tyr	Glu	Thr	Gly	Tyr	Ile	Lys	Phe	Ile
329			195						200				205
332	Lys	Glu	Ser	Phe	Trp	Phe	Asp	Phe	Phe	Pro	Glu	Pro	Glu
333		210					215					220	
336	Ser	Lys	Tyr	Leu	Met	Ile	Tyr	Lys	Asp	Asn	Glu	Thr	Leu
337	225					230					235		240
340	Thr	Ser	Gln	Ile	Glu	Val	Tyr	Leu	Thr	Thr	Lys		
341				245					250				

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